Title: HUMAN PROTEINS RESPONSIBLE FOR NEDJS ACTIVATION AND CONJUGATION

Filing Date: Herewith

Attorney Docket No.: MP197-057P1RCP1CN1M
Applicant: Vinvent Chau

Figure 1 of 9 1/9

ATGGCTGTTGATGGTGGGTGTGGGGACACTGGGAAGGT	45
M N TO C C C G D T G D W E G	90
CGCTGGAACCATGTAAAGAAGTTCCTCGAGCGATCTGGACCCTTC R W N H V K K F L E R S G P F	90
ACACACCCTGATTTCGAACCGAGCACTGAATCTCTCCAGTTCTTG	135
THPDFEPSTESLQFL	100
TTAGATACATGTAAAGTTCTAGTCATTGGAGCTGGCGGCTTAGGA	180
TGTGAGCTCCTGAAAAATCTGGCCTTGTCTGGTTTTAGACAGATT	225
CFT. KNLALSGEROI	070
CĂTGTTATAGĂTATGGÂCACTATAGĀTGTTTCCAĀTCTAAĀTAGG H V T D M D T I D V S N L N R	270
CAGTTTTTATTTAGGCCTAAAGATATTGGAAGACCTAAGGCTGAA	315
OFT. FRPKDIGRPKAE	260
GŤTGCTGCAGAATTTCTAAATGACAGAGTTCCTAATTGCAATGTA V A A E F L N D R V P N C N V	360
GTTCCACATTTCAACAAGATTCAAGATTTTAACGACACTTTCTAT	405
V P H F N K I O D F N D T F Y	450
CGACAATTTCATATTGTATĞTGGACTGGACTCTATCATCGCC R O F H I I V C G L D S I I A	450
R O F H I I V C G L D S I I A AGAAGATGGATAAATGGCATGCTGATATCTCTTCTAAATTATGAA	495
PPWTNGMI ISLLNYE	5.40
GATGGTGTCTTAGATCCAAGCTCCATTGTCCCTTTGATAGATGGG	540
D G V L D P S S I V P L I D G GGGACAGAAGGTTTTAAAGGAAATGCCCGGGTGATTCTGCCTGGA	585
CTECFKGNARVILPG	600
ATGACTGCTTGTATCGAATGCACGCTGGAACTTTATCCACCACAG	630
M T A C I E C T L E L Y P P Q GTTAATTTTCCCATGTGCACCATTGCATCTATGCCCAGGCTACCA	675
VNFPM(C*)TIASMPRLP	700
GÁACACTGTATTGAGTATGTAAGGATGTTTGCAGTGGCCTAAGGAG E H C I E Y V R M L Q W P K <u>E</u>	720
E H C I E Y V R M L Q W P R E CAGCCTTTTGGAGAAGGGGTTCCATTAGATAGATGATCCTGAA	765
OPFCEGVPIDGDDPE	010
CATATACAATGGATTTTCCAAAAATCCCTAGAGAGAGCATCACAA H I O W I F O K S L E R A S Q	810
TATAATATTAGGGGTGTTACGTATAGGCTCACTCAAGGGGTAGTA	855
VNTRGVTYRLTOGVV	000
AAAGAATCATTCCTGCAGTAGCTTCCACAAATGCAGTCATTGCA KRIIPAVASTNAVIA	900
K R I I P A V A S T N A V I A GCTGTGTGTGCACTGAGGTTTTTAAAATAGCCACAAGTGCATAC	945
AVCATEVEKIATSAY	000
ATTCCCTTGAATAATTACTTGGTGTTTAATGATGTAGATGGGCTG	990
mama Cama Ca Camarca a CCa Ca a a a a a cCA cCA cCA a cCA a a a a cCA cCA cCA a cCA a a a a cCA cCA cCA a cC	1035
V T V T F E A E R K E N C P A	1000
─────────────────────────────────────	1080
C S O L P O N I O F S P S A K CTACAGGAGGTTTTGGATTATCTAACCAATAGTGCTTCTCTGCAA	1125
	4450
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	1170
M K S P A I T A T L E G K N R ACACTTACTTACAGTCGGTAACCTCTATTGAAGAACGAAC	1215
T L Y L O S V T S I E E R T R CCAAATCTCTCCAAAACATTGAAAGAATTGGGGCTTGTTGATGGA	
CCAAATCTCTCCAAAACATTGAAAGAATTGGGGCTTGTTGATGGA	1260
PNLSKTLKELGEVDG	1305
Q E L A V A D V T T P Q T V L TTCAAACTTCATTTTACTTCTTAA 1329	
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FKLHFTS.	

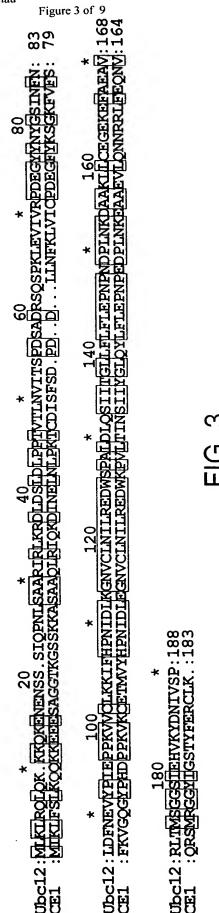
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Figure 2 of 9

2/9

+1 G G T K G S S K K A S A A O L R GGGCGGCACC AAGGGCACA GCAAGAAGG CCCGCCGTGG TTCCCGTCGT CGTTCTTCCG CAGCCGCCG CTCGACGCCT  +1 I O K D I N E L N L P K T C D I S TCCAGAAGGA CATAAACGAG CTGAACCTGC CCCAAGACGTG TGATATCAGC AGGTCTTCCT GTATTTGCTC GACCTGCC CCCAAGACGTG TGATATCAGC AAGAGTCTAG GTCTGCTGGA GGAGTTGAAG TTCGACCAGT ACACAGGACT  +1 F S D P D D L L N F K L V I C P D TCCAAGAGTC CAGACGACCT CCCTAACTTC AAGCCGAGTA AGACAGGACT  +1 TCTCCAGAAG GTCTGCTGGA GGAGTTGAAG TTCGACCAGT AGACAGGACT  +1 TGAGGGCTTC TACAAGAGTG GGAAGTTTGT GTTCAGACCAGT AGACAGGACT ACTCCCGAAG ATGTTCTCAC CCTTCAAACA CAAGTCAAAA TTCCACCCGG  +1 Q G Y P H D P F K V K C E T M V Y TCCCAATGG CGTACTAGGG GGGATCCACA CAAGTCAAAA TTCCACACTTAT TCCCAATGG CGTACTAGGG GGGAACCTC TGCCTCAACA TCCTCAGAGA GTGGGGTTGT AACTGGAGCT CCCCTTCCACA TCCCAGATA  +1 H P N I D L E G N V C L N I L R E 301 CACCCCAACA TTGACCTCGA GGGCAACCTC TGCCTCAACA TCCTCAGAGA GTGGGGTTGT AACTGGAGCT CCCGTTGCAG ACGGAGTTGT AGGAGTCTCT  +1 D W K P V L T I N S I I Y G L Q CTGACCTTC GGACCCCAAC CCCGTTGCAG ACGGAGTTGT AGGAGCTCCAC  +1 Y L F L E P N P D P L N K E A A 401 ATCTCTTCTT GGAGCCCAAC CCCGAAGACC CATAATTAATA CCGGACGCCA TAGAGAAGAA CCTCGGGTTG GGGCTCCTGG GTGACTTGTT GAGCAGCGCCA  +1 Y L F L E P N P D P L N K E A A 401 ATCTCTTCTT GGAGCCCAAC CCCGAAGACC CATAATTAATA CCGGACGCCA TAGAGAAGAA CCTCGGGTTG GGGCTCCTGG GTGACTTGACAA GGAGCCGCA  +1 M R G G Y I G S T Y F E R C L K 451 GAGGTCCTGC AGAACAACCG GCGCGCACAAAA CTCGTCTTGC ACGGCCCCAC CTCCAGGGGT GCTCACATCG GCTCCACCTA CTTTGAGCGCC TCCAGGACTTA  +1 M R G G Y I G S T Y F E R C L K 501 CATGCGGGGT GCTCACATCG GCTCCACCTA CTCTGCTCAGCGC TCCCGCGCAC  +1 M R G G Y I G S T Y F E R C L K 501 CATGCGGGGT GCTCACATCG GCTCCACCTA CTCTGCTCTG	+1	M I ATGATCA TACTAGT	K I AGC TCG	F TGTT ACAA	S L CTCGCT GAGCGA	K GAAGO CTTCO	Q Q CAGCAG STCGTC	K K AAGAAG TTCTTC	E E GAGG CCTCC	AGGA TCCT	S A GTCGGC CAGCCG
101 TCCĀGAGGA CATAAACGAG CTGAACCTGC CCAAGACGTG TGATATCAGC AGGTCTTCCT GTATTTGCTC GACTTGGACG GGTTCTGCAC ACTATAGTCG  +1 F S D P D D L L N F K L V I C P D 151 TTCTCAGATC CAGACGACCT CCTCAACTTC AAGCTGGTCA TCTGTCCTGA AAGAGTCTAG GTCTGCTGGA GGAGTTGAAG TTCGACCAGT AGACAGGACT  +1 E G F Y K S G K F V F S F K V G ACTCCCGAAG ATGTTCTCAC CCTTCAAACA CAAGTCAAAA TTCCACCGG  +1 Q G Y P H D P P K V K C E T M V Y 251 AGGGTTACCC GCATGATCCC CCCAAGGTGA AGTGTGAGACA TTCCACCGG  +1 P N I D L E G N V C L N I L R E 301 CACCCCACAA TTGACCTCGA GGGCAACGTC TGCCTCAACA TCCTCAGAGA GTGGGGTTGT AACTGGAGCT CCCGTTGCAA ACGGAGTTGT AGGAGTCTCT  +1 D W K P V L T I N S I I Y G L Q CCTGACCTTC GGTCAGGAAT GCTATTTGAG GTATTAAATA CCGGACGTCA  +1 Y L F L E P N P E D P L N K E A A 401 ATCTCTCTCT GGAGCCCAAC CCCGAGGAGC CACTGAACAA GGAGGCCCCA TAGAGAAAA CCTCCGGTTG GGGCTCCTTT GACACTTGT CCTCCGGCGT  +1 E V L Q N N N R R L F E Q N V Q R S 451 GAGGTCTGC AGAACAACCG GCGCGCTCTTT GACACTGTT TCCCCGGCGT  +1 E V L Q N N N R R L F E Q N V Q R S 451 GAGGTCTGC AGAACAACCG GCGCGCTCTTT GACACTGTT CCTCCGGCGT  +1 M R G G G Y I G S T Y F E R C L K 501 CATGCCGGG TGCCTTAACCC CCGAGGTGAT GAAACTCGCG ACGGACTTTA  +1 M R G G G Y I G S T Y F E R C L K 501 CATGCGGGGT GGCTACATCG GCTCCACCTA CTTTGAGCGC TGCACGTAC  +1 M R G G G Y I G S T Y F E R C L K 501 CATGCGGGGT GGCTACACTC CGGAGGTGAT GAAACTCGCG ACGGACTTTA  +1 M R G G G Y I G S T Y F E R C L K 501 CATGCGGGGT GGCTACACTC CGGAGGTGAT GAAACTCGCG ACGGACTTTA  +1 M R G G G Y I G S T Y F E R C L K 501 CATGCGGGGT GGCTACACTC CGGAGGTGAT GAAACTCGCG TGCCTGAAAT  -1 M R G G G Y I G S T Y F E R C L K 501 CATGCGGGGT GGCTACACTC CGGAGGTGAT GAAACTCGCG TGCCTGAAAT  -1 M R G G G Y I G S T Y F E R C L K 501 CATGCGGGGT GGCTACACTC CGGAGGTGAT GAAACTCGCG TGCCTGAAAT  -1 M R G G G Y I G S T Y F E R C L K 501 CATGCGGGGT GGCTACACTC CGGAGGTGAT GAAACTCGCG ACGGACTTTA  -1 M R G G G Y I G S T Y F E R C L K 501 CATGCGCCCA CCGAGGTGAT GAAACTCGCG ACGGACTTTA  -1 M R G G G Y I G S T Y F E R C L K 501 CATGCGCCCA CCGAGGTGAT GAAACTCGCG ACGGACTTTA  -1 M R G G G Y I G S T Y F E R C L K 501 CATGCGCCCA CCGAGGT		GGGCGGC	ACC	AAGG	GCAGCA	GCAAG	BAAGGC	GTCGGC	CGGCG	CÃGC	TGCGGA
151 TTCTCAGATC CAGACGACT CCTCAACTTC AAGCTGGTCA TCTGTCCTGA AAGAGACTTAG GTCTGCTGGA GGAGTTGAAG TTCGACCAGT AGACAGGACT  +1 E G F Y K S G K F V F S F K V G ACTCCCGAAG ATGTTCTCAC CCTTCAAACA CAGATTTT AAGGTGGGCC ACTCCCGAAG ATGTTCTCAC CCTTCAAACA CAGATCAAAA TTCCACCCGG  +1 Q G Y P H D P P K V K C E T M V Y ACTCCCAATGGG CGATGATCCC CCCAAGGTGA AGTGTGAGAC AATGGTCTAT TCCCAATGGG CGTACTAGGG GGGTTCCACT TCACACTCTG TTACCAGATA TCCCCAATGGG CGTACTAGGG GGGTTCCACT TCACACTCTG TTACCAGATA TCCCCAATGAG CGGCAACGTC TGCCTCAACA TCCTCAGAGA GTGGGGGTTGT AACTGGAGCT CCCGTTGCAG ACGGAGTTGT AGGAGTCTCT  +1 D W K P V L T I N S I I Y G L Q ACTGGACGTC CCTGACCTTC GGTCAGGAAT GCTATTTGAG GTATTAAAATT CCGGACGTCATC CCTGACCTTC GGTCAGGAAT GCTATTTGAG GTATTAAAATA CCGGACGTCA TAGAGAAGAA CCTCGGGTGAG GGGCTCCTGG GTGACTTGTT CCTCCGGCGT TAGAGAAGAA CCTCGGGTTG GGGCTCCTGG GTGACTTGTT CCTCCGGCGT TAGAGAAGAA CCTCGGGTTG GGGCTCCTGG GTGACTTGTT CCTCCGGCGT TAGAGAAGAA CCTCGGGTTG GGGCTCCTGG GTGACTTGTT CCTCCGGCGT TAGAGAAGAA CTCGTCTTGTT CCTCCGGCGT TAGAGAAAAACAC CATGAACAA GGAGGCCGCA TAGAGAAGAA CCTCGGGTTG GGGCTCCTGG GTGACTTGTT CCTCCGGCGT TAGAGAAAAACAC CCCGAGGACC CACTGAACAA GGAGGCCGCA TAGAGAAGAA CCTCGGGTTG GGGCTCCTGG GTGACTTGTT CCTCCGGCGT TAGAGAGAAGAA CCTCGGGTTG GGGCCCCAAC CCCGAGGACC CACTGAACAA GGAGGCCGCA TAGAGAAAACAC CCCGAGGACC CACTGAACAA GGAGGCCGCA TAGAGAAAACAC CCCGAGGACC CACTGAACAA GGAGGCCGCA TAGAGAAAACAC CCCGAGGACC CACTGAACAA CTCGTCTTGC ACGACCCCA CCTCACCACAA CTCGTCTTGC ACGACCTCA CTTTGAGCGC TGCCTGAAAACAA CTCGTCTTGC ACGACCTCA CTTTGAGCGC TGCCTGAAAACAA CTCGTCTTGC ACGACCTTAAACAC CTATGTAGCCC CATGAACAA CTCGTCTTGAAACACCC ACGACCTTAAACAC CTCGTCTTGC ACGACCTCA CTTTGAGCGC TGCCTGAAAACAA CTCGTCTTGC ACGACCTTAAACACAC CCGAGGTGGAT GAAACACCCG ACGACCTTTA CTTTGAGCGC TGCCTGAAAACACCG GCGCGCGCGCAACAA CTCGTCTTGC ACGGCCCCA ACGACCTTAAACACCC CCGAGGTGGAT GAAACCTCGCG ACCGACCTTAAACACCC CCGAGGTGGAT GAAACCTCGCG ACGACCTTTAAACACCCCCAAC CCGAGGTGGAT GAAACCTCGCG ACGGACTTTAAACACCCCCAAC CCGAGGTGGAT GAAACCTCGCG ACGGACTTTAACCCCCCACCAC CCGAGGTGGAT GAAACCTCGCG ACGGACTTTAACCCCCACCACCAC CCGAGGTGGAT GAAACCTCCGCACCACCACCACCACCACCACCACCACCA	+1 101	TCCÃGAA	GGA	CATA	AACGAG	CTGA	ACCTGC	CCAAG	ACGTG	TGAT	ATCAGC
201 TGAGGGCTTC TACAAGAGTG GGAAGTTTGT GTTCAGTTTT AAGGTGGCC ACTCCCGAAG ATGTTCTCAC CCTTCAAACA CAAGTCAAAA TTCCACCGG  +1 O G Y P H D P P K V K C E T M V Y 251 AGGGTTACCC GCATGATCCC CCCAAGGTGA AGTGTGAGAC AATGGTCTAT TCCCAATGGG CGTACTAGGG GGGTTCCACT TCACACTCTG TTACCAGATA  +1 H P N I D L E G N V C L N I L R E 301 CACCCCAACA TTGACCTCGA GGGCAACGTC TGCCTCAACA TCCTCAGAGA GTGGGGTTGT AACTGGAGCT CCCGTTGCAG ACGGAGTTGT AGGAGTCTCT  +1 D W K P V L T I N S I I Y G L Q 351 GGACTGGAAG CCAGTCCTTA CGATAAACTC CATAATTTAT GGCCTGCAGT CCTGACCTTC GGGTCAGGAAT GCTATTTGAG GTATTAAATA CCGGACGTCA  +1 Y L F L E P N P E D P L N K E A A 401 ATCTCTTCTT GGAGCCCAAC CCCGAGGACC CACTGAACAA GGAGGCCGCA TAGAGAAGAA CCTCGGGTTG GGGCTCCTGG GTGACTTGTT CCTCCGGCGT  +1 E V L Q N N R R L F E Q N V Q R S 451 GAGGTCCTGC AGAACAACG GCGCTGTTT GAGCAGAACG TGCAGCGCTC CTCCAGGACG TCTTGTTGGC CGCCGACAAA CTCGTCTTGC ACGTCGCGAG  +1 M R G G Y I G S T Y F E R C L K 501 CATGCGGGGT GGCTACATCG GCTCCACCTA CTTTGAGCGC TGCCTGAAAT GTACGCCCCA CCGATGTAGC CGAGGTGAT GAAACTCGCG ACGGACTTTA  +1 M R G G Y I G S T Y F E R C L K 501 CATGCGGGGT GGCTACATCG GCTCCACCTA CTTTGAGCGC TGCCTGAAAT GTACGCCCCA CCGATGTAGC CGAGGTGGAT GAAACTCGCG ACGGACTTTA  +1 * 551 AG	+1 151	TTCTCAG	ATC	CAGA	CGACCI	CCTC	AACTTC	AAGCT	GTCA	TCTG	TCCTGA
251 ĀGGGTTACCC GCATGATCCC CCCAAGGTGA AGTGTGAGAC AATGGTCTAT TCCCAATGGG CGTACTAGGG GGGTTCCACT TCACACTCTG TTACCAGATA  +1 H P N I D L E G N V C L N I L R E 301 CACCCCAACA TTGACCTCGA GGGCAACGTC TGCCTCAACA TCCTCAGAGA GTGGGGTTGT AACTGGAGCT CCCGTTGCAG ACGGAGTTGT AGGAGTCTCT  +1 D W K P V L T I N S I I Y G L Q 351 GGACTGGAAG CCAGTCCTTA CGATAAACTC CATAATTTAT GGCCTGCAGT CCTGACCTTC GGTCAGGAAT GCTATTTGAG GTATTAAATA CCGGACGTCA  +1 Y L F L E P N P E D P L N K E A A 401 ATCTCTTCTT GGAGCCCAAC CCCGAGGACC CACTGAACAA GGAGGCCGCA TAGAGAAGAA CCTCGGGTTG GGGCTCCTGG GTGACTTGTT CCTCCGGCGT  +1 E V L Q N N R R L F E Q N V Q R S 451 GAGGTCCTGC AGAACAACCG GCGGCTGTTT GAGCAGAACG TGCAGCGCTC CTCCAGGACG TCTTGTTGGC CGCCGACAAA CTCGTCTTGC ACGTCGCGAG  +1 M R G G Y I G S T Y F E R C L K 501 CATGCGGGGT GGCTACATCG GCTCCACCTA CTTTGAGCGC TGCCTGAAAT GTACGCCCCA CCGATGTAGC CGAGGTGGAT GAAACTCGCG ACGACTTTA  +1 * 551 AG	+1 201	TGAGGG	CTTC	TACA	AGAGT	GGAA	STTTGT	GTTCA	STTTT	AAGG	TGGGCC
301 CACCCCAACA TTGACCTCGA GGGCAACGTC TGCCTCAACA TCCTCAGAGA GTGGGGTTGT AACTGGAGCT CCCGTTGCAG ACGGAGTTGT AGGAGTCTCT  +1 D W K P V L T I N S I I Y G L Q  351 GGACTGGAAG CCAGTCCTTA CGATAAACTC CATAATTTAT GGCCTGCAGT CCTGACCTC GGTCAGGAAT GCTATTTGAG GTATTAAATA CCGGACGTCA  +1 Y L F L E P N P E D P L N K E A A  401 ATCTCTTCTT GGAGCCCAAC CCCGAGGACC CACTGAACAA GGAGGCCGCA TAGAGAAGAA CCTCGGGTTG GGGCTCCTGG GTGACTTGTT CCTCCGGCGT  +1 E V L Q N N R R L F E Q N V Q R S  451 GAGGTCCTGC AGAACAACCG GCGGCTGTTT GAGCAGAACG TGCAGCGCTC CTCCAGGACG TCTTGTTGGC CGCCGACAAA CTCGTCTTGC ACGTCGCGAG  +1 M R G G G Y I G S T Y F E R C L K  501 CATGCGGGGT GGCTACATCG GCTCCACCTA CTTTGAGCGC TGCCTGAAAT GTACGCCCCA CCGATGTAGC CGAGGTGGAT GAAACTCGCG ACGGACTTTA  +1 *  551 AG	+1 251	ĀGGGTT	ACCC	GCAT	'GATCC	CCCA	AGGTGA	AGTGT	<b>GAGAC</b>	AATG	GTCTAT
351 GGACTGGAAG CCAGTCCTTA CGATAAACTC CATAATTTAT GGCCTGCĀGT CCTGACCTTC GGTCAGGAAT GCTATTTGAG GTATTAAATA CCGGACGTCA  +1 Y L F L E P N P E D P L N K E A A 401 ATCTCTTCTT GGAGCCCAAC CCCGAGGACC CACTGAACAA GGAGGCCGCA TAGAGAAGAA CCTCGGGTTG GGGCTCCTGG GTGACTTGTT CCTCCGGCGT  +1 E V L Q N N R R L F E Q N V Q R S GAGGTCCTGC AGAACAACG GCGGCTGTTT GAGCAGAACG TGCAAGCGCTC CTCCAGGACG TCTTGTTGGC CGCCGACAAA CTCGTCTTGC ACGTCGCGAG  +1 M R G G G Y I G S T Y F E R C L K 501 CATGCGGGGT GGCTACATCG GCTCCACCTA CTTTGAGCGC TGCCTGAAAT GTACGCCCCA CCGATGTAGC CGAGGTGGAT GAAACTCGCG ACGGACTTTA  +1 * 551 AG											
401 ATCTCTTCTT GGAGCCCAAC CCCGAGGACC CACTGAACAA GGAGGCCGCA TAGAGAAGAA CCTCGGGTTG GGGCTCCTGG GTGACTTGTT CCTCCGGCGT  +1 E V L Q N N R R L F E Q N V Q R S 451 GAGGTCCTGC AGAACAACCG GCGGCTGTTT GAGCAGAACG TGCAGCGCTC CTCCAGGACG TCTTGTTGGC CGCCGACAAA CTCGTCTTGC ACGTCGCGAG  +1 M R G G Y I G S T Y F E R C L K 501 CATGCGGGGT GGCTACATCG GCTCCACCTA CTTTGAGCGC TGCCTGAAAT GTACGCCCCA CCGATGTAGC CGAGGTGGAT GAAACTCGCG ACGGACTTTA  +1 * 551 AG	301	CACCCC	AACA	TTGA	CCTCG	GGGC	AACGTC	TGCCT	CAACA	TCCT	CAGAGA
451 GAGGTCCTGC AGAACAACCG GCGGCTGTTT GAGCAGAACG TGCAGCGCTC CTCCAGGACG TCTTGTTGGC CGCCGACAAA CTCGTCTTGC ACGTCGCGAG  +1 M R G G Y I G S T Y F E R C L K 501 CATGCGGGGT GGCTACATCG GCTCCACCTA CTTTGAGCGC TGCCTGAAAT GTACGCCCCA CCGATGTAGC CGAGGTGGAT GAAACTCGCG ACGGACTTTA  +1 * 551 AG	301	CACCCC GTGGGG D W GGACTG	AACA FTGT K SAAG	TTGA AACT P CCAG	CCTCGI GGAGC'I V L	GGGCA CCCGA T I	AACGTC TTGCAG  N S AAACTC	TGCCTO ACGGAO I CATAA	CAACA GTTGT  I Y ITTAT	TCCT AGGA G GGCC	CAGAGA GTCTCT L Q TGCAGT
501 CATGCGGGGT GGCTACATCG GCTCCACCTA CTTTGAGCGC TGCCTGAAAT GTACGCCCCA CCGATGTAGC CGAGGTGGAT GAAACTCGCG ACGGACTTTA +1 * 551 AG	301 +1 351 +1	CACCCA GTGGGGT  D W GGACTGA CCTGACC  Y L ATCTCT	AACA TTGT K SAAG CTTC F L ICTT	P CCAG GGTC	CCTCGA GGAGCT V L GTCCTTA CAGGAAT P N	T I CGATA	AACGTC TTGCAG N S AAACTC TTTGAG E D AGGACC	TGCCTC ACGGAC  I CATAA! GTATTI P L CACTGI	CAACA GTTGT I Y ITTAT AAATA N K AACAA	G G G G C C C C G G C C G G C C G G C C G G C C G G C C C G G C C C C C C C C C C C C C C C C C C C C	CAGAGA GTCTCT L Q TGCAGT ACGTCA A A
551 AG	301 +1 351 +1 401 +1	D W GGACTGC CCTGACC ATCTCTT TAGAGA	AACA FTGT  K SAAG CTTC F L FCTT AGAA  L CTGC	P CCAG GGTC E GGAG CCTC	CCTCGA GGAGCT V L GTCCTTA CAGGAAT P N GCCCAAC GGGGTTC	T I CGATA CGATA CCCCG GGGGC CCCCGGGGGGC CCCGGGGGGCC	AACGTC ITGCAG N S AAACTC ITTGAG E D AGGACC ICCTGG L F CTGTTT	TGCCTC ACGGAC  CATAA! GTATTA CACTGAC GTGAC E Q GAGCA	CAACA GTTGT I Y ITTAT AAATA N K AACAA ITGTT N GAACG	TCCT AGGA GGCC CCGG E GGAG CCTC	CAGAGA GTCTCT L Q TGCAGT ACGTCA A A GCCGCA CCGCCA
	301 +1 351 +1 401 +1 451 +1	D W GGACTGC CCTGACC ATCTCTTAGAGAC E V GAGGTCC CTCCAGC	K GAAG CTTC F L TCTT AGAA CTGC GACG	P CCAG GGTC E GGAG CCTC AGAA TCTT	CCTCGA GGAGCT V L STCCTTA AGGAAT CCCCAAC GGGTTC GTTGGC	GGGCZ CCGGC CCGGCGCGCGCGCGCGCGCGCGCGCGCG	AACGTC TTGCAG  N S AAACTC TTTGAG  E D AGGACC ICCTGG  L F CTGTTT GACAAA  T Y CACCTA	I CATAA! GTATT CACTG GTGAC! E Q GAGCAC CTCGT CTTTG	CAACA GTTGT  I Y ITTAT AAATA  N K AACAA ITGTT  N GAACG CTTGC  E R AGCGC	GGCC CCGG GGAG CCTC TGCA ACGT	CAGAGA GTCTCT L Q TGCAGT ACGTCA CGCCGCA CGGCGT CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG



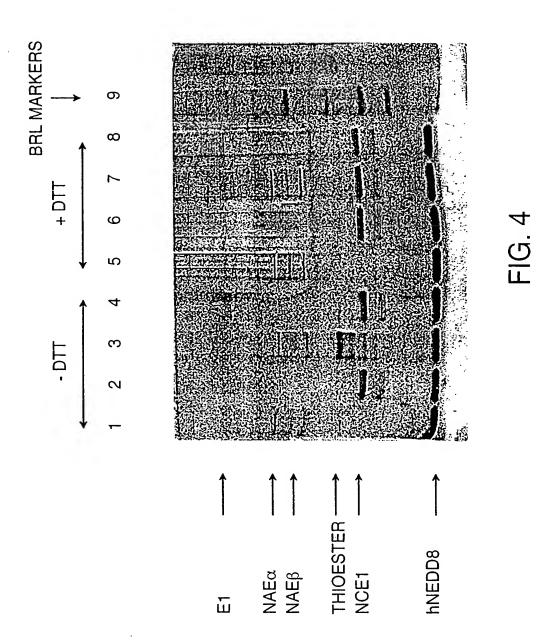
3/9

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Figure 4 of 9 4/9



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Figure 5 of 9 5/9

+1 1	M ATGC TACG	TAP	CGC	TF	AGC	<b>\AG</b>	TAA	ACI	'GA	AG	CGT	GAC	GAI	'GG'I	'C	TCA	ÃΑ	GĞG	TC
51 51	R CCGG GGCC	AČC		GÖ	CCA	CAG		CCG	FAC	TC	GAC		GAC	GGI	T		ĠŤ	GAG	AG
+1 101	D K ACAA TGTT	ATI	GCI	TO	STT	AAA	GAG	GTT	'GC	AG	AAC	TTG	AAC	CTA	\A	I TTT AAA	AC	P CTT GAA	ĠT
+1	T	С	ĸ	V	н	F	P	r	)	P	N	Hir	L ndII	Ι	C	;	F	Q	L
151	ACAT TGTA	GTA CA	AAA OTTT	TO	GCA'	TTT AAA	TCC AGG	TG! ACI	ATC TAG	CA GT	AAC TTG	AAG	CTI	'CA'	TT AA	GTT CAA	TT	CAG GTC	CT GA
201 	T AACA TTG1	V GTA CA	AACC	C	CAG	ATG	E AGG TCC	GTT	'AC	TA	CCĀ	GGG	TGC CACC	AAA	\A	TTT	Q CA GT	F GTT CAA	TG AC
	E TAAAC	TGI	AAGI	T	CCC	GAT	GCG	TAC	CAA	CA		TGC	CTC	CCCF	A	AGT	'GA	<b>TAA</b>	'GC
+1 301					CTG	<b>GCA</b>		CAZ	<b>ACA</b>	TC	ACA		SACI			AAA			CT
351		TTT	ATTO	3 A	GAG.	AAC	ATT	CA	TTP	'GA	G TGG ACC	CAC	CTG	CTC	3G	GCI	P 'CC	CAC	AA
	R I GAAC CTTC	AT:		G		GŤC		TG	<b>GG</b> G	AT		ACT		ľŦĠľ			TG		
+1	L	N	F	D	D	F	L	1	<b>N</b>	I	E		A ?st]		F	I	Н	L	R
451	TTGA AACT			-															
	D GGA CCT	CAAC	<b>GGA</b> (	3 G	ACT	TCC	GGA	ATA	AAA	GT	GGA	TG	ACTA	ACA	ГC	AAA	LCG	TTF	TG
+1 551	A I CCA GGT	SAT	GA													*****			

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Figure 6 of 9 Figure 6 of 9 6/9

ACTIVATION AND CONJUGATION
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Attorney Docket No.: MP197-057P1RCP1CN1M
Applicant: Vinvent Chau

Figure	7 of 9
00000040000000000000000000000000000000	7
80 DLINE PNKLHCF DENFTEL ENNIMOW EGDLYNW GDDLFHW GDDLFHW GDDLFHW GDDLFHW GDDLFHW GDDLFHW GDNIYEW CDNIYEW CDNIFEW CDNIFEW CDNIFEW CSNIFE	160 EDWREVITINS TGWALTINS TGWALTRITKD DOWNAAMTIRT RWSPITYDVSS SERWNPICONVRI SOWSPALTISK SOWSPALTISK SOWSPALTISK SOWSPALTISK ENWREPALTISK DNWSPALTISK DNWSPALTISK DNWSPALTISK ENWREPALTISK ENWREPALTISK ENWREPALTISK ENWREPALTISK DTWREVETT
* DISFSDED. KVHFED. NOIKVDLV. VSGAPS. VSGAPS. VSGAPS. CSAGPV.	160 EDWR TOWNS SGELLPSERWN SOWS SOWS SOWS SYEKPEERWH EKWK EKWK DEWR
ANLPCTC. KSEETSKN. EDPPAG. EDPPAG. EDPPAG. EDPPAG. EDPPAG. EDPPAG. RDPPAG. RDPPAG. RDPPAG. RCGMKN. KKPPPY. KKPPPY. KKPPPY. KKPPPY. KKPPPY.	* SHSIDG. SPYDDPQ. SPYDDPQ. SPYDDPQ. SPYDDPQ. SPYDDPQ.
60 OKEVAELE WKEVAELE WRDFYRLO MRDFYRLO HKELNDLA HKELNDLA OKELSDLO OKELEDLO OKELEDLO OKELEDLO OKELEDLO OKELEDLO OKELEDLO KROLAELN RADTDVVK AOERKAWR	1. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2.
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EGG · · · · · · · · · · · · · · · · · ·	
MITLESLER MITLASKLERD SSSSSNQQTEKET	100 * GKEVESETKVGGGS GKEVESETKVGGGS GKEOFETEVPDAN GKEVELTIEFTEEN GKEVELTIHFPTDN GKEVELTIHFTPTDN GKEVELTIHF
	100 100 100 100 100 100 100 100
* 20 MITLASKLKRD MITLASKLKRD MSDDDSRASTSSSSSSNQQTEKET	* 100 *  KLVIC PDEGFYKSGKEVFSFKVGQG OLTVT PDEGYYGGKEVFETEVPDA RGEIAGPEDTPYEGGRYGLEIKIPET NAVIEGPEGTPFEDGIEKLVIEFSEE NAVIEGPEGTPFEDGIEKLTIEFTEE EVALEGPENTYYEGGYEKTITHFPTD OATIMGPNDSPYGGWEELTIHFPTD OATIMGPNDSPYGGWEELTIHFPTD OATIMGPNDSPYGGWEELTIHFPTD OATIMGPNDSPYGGWEELTIHFPTD OATIMGPPDSAYGGGWEELTIHFPTD RSTILLGPPGSVYEGGWEELTIHFPTD RSTILLGPPGSVYEGGWEELTIHFPTD RSTILLGPPGSVYEGGWEELTIHFPTD SGILV PDNPPYDKGMEELTIHFPTD FYLILGPPDTLYEGGWEKAHLTFPRD VVKFYGDGGTPYEGGWEKAHLTFPRD VVKFYGDGGTPYEGGWEKAHLTFPED VGTIHGAAGTVYEDIRYKLSLEFPSG HVVIAGPODSPFEGGTEKLELFLPEE
NCE1 NCE2 UBC1 UBC2A UBC2A UBSB UBSB UBSB UBSB UBSB UBSB UBSB UBS	NCE1 NCE2 UBC2b UBC2a UBS2B UBS2B UBSC UBCH6 UBCH6 UBCH6 UBCH6 UBCH10 UBCH10

7/9

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11111111111111111111111111111111111111	236 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	8/9
# JEDRNAVIVA JYCVKTKAPA	*	
240 IENILCAMO SVPTTLAE SVPTTLAE STOSSESS	320	
YFERCLK SSPEYTKKIE NDAERDGVKV ND ND IKEQEEGTGD	*	
220 SMRGGYIGST YIKRYAR WAHVYAGAPV IVIOSWND.S IVIOSWNDC IIRKOVLGTK WTOKYAM WTOKYAM WTOKYAM WTOKYAM WTOKYATEEA OAKKEAPS IYSKOVTSOE IYSKOVTSOE IYSKOVTSOE IYSKOVTSOE IYSKOVTSOE IYSKOVTSOE IYSKOVTSOE IYSKOVTSOE	g ::::::::::::::::::::::::::::::::::::	
220 EEONVORSMRGGY1 ERNKVDDYIKRYAR EKCTARLWAHVYAG EKCTARLWAHVYAG EKCTARLWAHVYAG EKCTARLWAHVYAG EKCTARLWAHVYAG INRIAREWTOKYAM INRIAREWTOKYAM INRAREWTOKYAM INRARAOAKKFAD INGETYSKOVTI INRARAWTRIYAM INRARAWTRIYAM INRARAWTRIYAM	00	<b>2</b>
* ** ** ** ** ** ** ** ** ** ** ** ** *	* · · · · · · · · · · · · · · · · · · ·	FIG.
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*  NECONSTRUCTION AND THE PROPERTY OF THE PROP		
	* TILLSN. EDGEVE	
* 180 IIYGLOYDETEP. VVWGLNSDERDLL VLISIQADLAAA. ILTSIQSDLDEP. ILTSVISDLDEP. ILTSVISDLDEP. VLISICSDLCDP. VLISICSDLCDP. VLISICSDLCDP. VLISICSDLCDP. VLISICSDLCDP. VLISICSDLCDP. VLISICSDLCDP. VLISICSDLCDP. VLISICSDLCDP. ITTSVISMLADP. ITTSVISMLA	260 * LSSKSWDVETATELLLSN  PDEGSDLFYDDYYEDGEVEEEADSCF  QDWEL	
*  *  *  *  *  *  *  *  *  *  *  *  *	PDEGSI	
NCE1 NCE2 NCE2 UBC1 UBC2a Cdc34a Cdc34a UBC3 UBC4A UBC4A UBCH(8) UBCH(8)	NCE1 NCE2 UBC1 UBC2a Cdc34a UBSB UBSB UBSB UBSB UBSB UBSB UBSB UBS	

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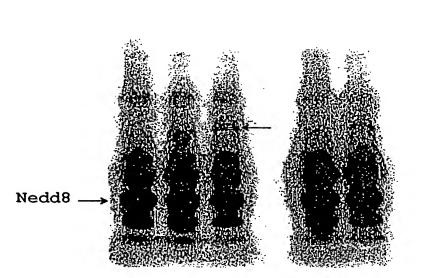
Applicant: Vinvent Chau

Figure 9 of 9 9/9

	340	*	360	*	
NCE1	·				: -
NCE2	:		• • • • • • • • • •		: -
UBC1	·		• • • • • • • • • • •		: -
UBC2b	• • • • • • • • •		• • • • • • • • • • • •		: -
UBC2a	• • • • • • • • • •	• • • • • • •	• • • • • • • • • • • •	• • • • • • • • •	: -
Cdc34a UB5B		• • • • • • • •	• • • • • • • • • • • •	• • • • • • • • •	: -
UB5C	•	• • • • • • •	• • • • • • • • • • •	• • • • • • • • •	· · · · · · · · -
UB5A	• • • • • • • • •	• • • • • • •	• • • • • • • • • • •	• • • • • • • •	
UbcH6	• • • • • • • • •	• • • • • • • •	• • • • • • • • • • •	• • • • • • • • •	
UbcH7	• • • • • • • • •	• • • • • • • •	• • • • • • • • • • • • •	• • • • • • • •	
UbcH8				• • • • • • • •	• • • • •
UBE2G					· · · · · · -
UBCH(8)	•		••••		· · · · · · · · -
UBC9	• • • • • • • • •		• • • • • • • • • •	• • • • • • • •	
UBCH10	:		· • • • • • • • • • • • • • • • • • • •		
UBC13	<b>:</b>				: -

FIG. 7C

5



LANE 1: NO NCE LANE 2: + NCE1

LANE 3: + NCE2; ARROW INDICATES Nedd8 THIOESTER OF NCE2

LANE 4: SAME AS LANE 2 BUT + DTT LANE 5: SAME AS LANE 2 BUT + DTT

1

2